Listing of Claims:

The following listing of claims replaces all prior versions and listings of claims in the application. Please note that "Original" claims refer to claims as presented in International Application PCT/DK2003/000632.

1. (Original) A Factor VII (FVII) or Factor VIIa (FVIIa) polypeptide variant having an amino acid sequence comprising 1-15 amino acid modifications relative to human Factor VII (hFVII) or human Factor VIIa (hFVIIa) having the amino acid sequence shown in SEQ ID NO:1, wherein said variant sequence comprises a substitution in at least one position selected from the group consisting of L39, I42, S43, K62, L65, F71, E82 and F275,

with the proviso that said variant is not
[K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or
[A1Y+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or
[A1Y+A3S+F4GK+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or
[A1Y+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or
[A1Y+A3S+F4GK+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or [A3S+F4GK+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or
[A3S+F4GK+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or
[L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or
[I42N]hFVII/hFVIIa or [I42S]hFVII/hFVIIa or [I42A]hFVII/hFVIIa or
[I42Q]hFVII/hFVIIa.

2. (Original) The variant according to claim 1, wherein said variant sequence comprises at least one substitution selected from the group consisting of L39E, L39Q, L39H, I42R, S43H, S43Q, K62E, K62R, L65Q, L65S, F71D, F71Y, F71E, F71Q, F71N, E82Q, E82N, E82K and F275H,

with the proviso that said variant is not
[K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or
[A1Y+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or
[A1Y+A3S+F4GK+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or

[A1Y+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or [A1Y+A3S+F4GK+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or [A3S+F4GK+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or [A3S+F4GK+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or [L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa.

3. – 6. (Cancelled)

7. (Currently Amended) The variant according to ~~any of claims 1-6~~ claim 1, wherein said variant comprises at least two substitutions selected from the group consisting of L65Q, F71Y, K62E and S43Q.

8. – 12. (Cancelled)

13. (Currently Amended) The variant according to ~~any of claims 1-12~~ claim 1, wherein said variant comprises at least one amino acid modification in the Gla domain.

14. (Original) The variant according to claim 13, wherein said at least one modification in the Gla domain comprises a substitution in at least one position selected from the group consisting of P10, K32, D33 and A34.

15. – 24. (Cancelled)

25. (Currently Amended) The variant according to ~~any of the preceding claims~~ claim 1, wherein at least one amino acid residue comprising an attachment group for a non-polypeptide moiety has been introduced in a position located outside the Gla domain.

26. (Original) The variant according to claim 25, wherein at least one non-polypeptide moiety is covalently attached to at least one of said attachment groups.

27. (Original) The variant according to claim 26, wherein said non-polypeptide moiety is a sugar moiety.

28. (Original) The variant according to ~~any of claims 25-27~~ claim 25, wherein said attachment group is a glycosylation site.

29. (Cancelled)

30. (Currently Amended) The variant according to claim ~~29~~ 28, wherein said glycosylation site is introduced by substitution and said introduced glycosylation site is an *in vivo* glycosylation site.

31. (Cancelled)

32. (Original) The variant according to claim 30, wherein said introduced *in vivo* glycosylation site is an N-glycosylation site.

33. – 34. (Cancelled)

35. (Currently Amended) The variant according to ~~any of claims 32-34~~ claim 32, wherein said N-glycosylation site is introduced by a substitution selected from the group consisting of A51N, G58N, G48N+S60T, T106N, K109N, G124N, K143N+N145T, A175T, I205S, I205T, V253N, T267N, T267N+S269T, S314N+K316S, S314N+K316T, R315N+V317S, R315N+V317T, K316N+G318S, K316N+G318T, G318N, and D334N ~~and combinations thereof~~.

36. – 46. (Cancelled)

47. (Currently Amended) The variant according to ~~any of the preceding claims~~ claim 1, wherein said variant further comprises at least one modification in a position selected from the group ~~consisiting~~ consisting of 157, 158, 296, 298, 305, 334, 336, 337 and 374.

48. – 49. (Cancelled)

50. (Currently Amended) The variant according to ~~any of the preceding claims~~ claim 1, wherein said variant is in its activated form.

51. (Currently Amended) A nucleotide sequence encoding ~~a~~ the variant ~~as defined in any of claims 1-50~~ according to claim 1.

52. (Cancelled)

53. (Currently Amended) A host cell comprising ~~a~~ the nucleotide sequence ~~as defined in~~ according to claim 51 ~~or an expression vector as defined in claim 52~~.

54. (Original) The host cell according to claim 53, wherein said host cell is a gammacarboxylating cell capable of *in vivo* glycosylation.

55. (Currently Amended) A pharmaceutical composition comprising ~~a~~ the variant ~~as defined in any of claims 1-50~~ according to claim 1, and a pharmaceutical acceptable carrier or excipient.

56. – 61. (Cancelled)

62. (Currently Amended) A method for treating a mammal having a disease or a disorder wherein clot formation is desirable, comprising administering to a mammal in need thereof an effective amount of ~~the variant as defined in any of claims 1-50 or~~ the pharmaceutical composition ~~as defined in~~ according to claim 55.

63. (Original) The method according to claim 62, wherein said disease or disorder is selcted from the group consisting of hemorrhage; uncontrolled bleedings, such as trauma; cirrhosis; thrombocytopenia; haemophilia A and haemophilia B.

64. – 66. (Cancelled)